GNE.3030R1C6

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant	:	Goddard et al. (as amended)
Appl. No.	:	10/036,063
Filed	:	December 26, 2001
For	:	ANTIBODIES TO POLYPEPTIDES THAT INDUCE CELL PROLIFERATION (as amended)
Examiner	:	Kolker, Daniel E.
Group Art Unit	:	1646

DECLARATION UNDER 37 CFR §1.131

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

We declare and state as follows:

1. We are the inventors of the invention claimed in the above-captioned patent application.

2. During the time period in which we participated in the events and activities described herein, we were employed by Genentech, Inc., the assignee of the above-captioned application.

3. All of the events and activities described herein were performed by us personally, or by others at our direction as part of our duties as employees of Genentech, Inc.

4. The invention claimed in the above-captioned patent application was conceived and reduced to practice in the United States prior to November 18, 1999 as described below.

5. Prior to November 18, 1999, we conceived of the invention claimed in the above-captioned patent application. This is demonstrated by the attached sequence printout (Exhibit A), which was generated prior to November 18, 1999, and which shows the complete sequence of the nucleic acid having the sequence of SEQ ID NO: 56. The attached printout also shows the complete sequence of the polypeptide which has the sequence of SEQ ID NO: 57. As evidenced by the sequence printout, we were in possession of the complete nucleic acid and amino acid sequences prior to November 18, 1999.

6. The date deleted from Exhibit A is prior to November 18, 1999. This date was redacted pursuant to M.P.E.P. § 715.07. The date that remains is the date the report was printed, April 28, 2005.

7. After these initial experiments, we diligently reduced the claimed subject matter to practice by working to express and purify the encoded polypeptide and to run it systematically through many assays. The cDNA was deposited with the American Type Culture Collection (ATCC) on April 20, 1999 and assigned ATCC no. 203948. The protein of interest was assigned a "protein inventory

number" (*e.g.*, PIN1205-1), and this protein is a polypeptide having the sequence of SEQ ID NO:57, and is encoded by SEQ ID NO: 56.

8. Exhibit B shows that the protein lot designated PIN1205-1 was delivered to James Pan on a date prior to November 18, 1999 in order to perform assay ASY92, called "Mouse Mesangial Cell proliferation Assay." Also, as shown in Exhibit B, the assay was completed on a date prior to November 18, 1999. Exhibit B also shows that the tested polypeptides tested positive ("All Positives"), thereby confirming the ability of the encoded polypeptide to induce mesangial cell proliferation. Thus, actual reduction to practice occurred on a date prior to November 18, 1999.

9. The dates deleted from Exhibit B all are prior to November 18, 1999. These dates were redacted pursuant to M.P.E.P. § 715.07. The date that remains is the date the report was printed, April 28, 2005.

10. We worked with the Genentech, Inc. patent department to prepare a provisional patent application, which included the sequences of SEQ ID NO:56 and SEQ ID NO:57, and described how to make and use antibodies to the sequences of SEQ ID NO:57. That application was filed on April 21, 1999 as U.S. Provisional Application No. 60/130,359.

11. After reducing the invention to practice, we worked with the Genentech, Inc. patent department to prepare a non-provisional patent application, which included the sequences of SEQ ID NO:56 and SEQ ID NO:57, as well as the data showing the ability to induce mesangial cell proliferation. That application was filed on March 1, 2000 as PCT/US00/05601.

11. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By: A. Goddard
Audrey Goddard

Date: June 7/05

By: _____
Paul J. Godowski

Date: _____

By: _____
Austin L. Gurney

Date: _____

By: _____
James Pan

Date: _____

By: _____
Colin K. Watanabe

Date: _____

By: _____
William I. Wood

Date: _____

1723199
052005

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By: _____ Date: _____
Audrey Goddard

By: Paul J. Godowski Date: 5/31/05
Paul J. Godowski

By: _____ Date: _____
Austin L. Gurney

By: _____ Date: _____
James Pan

By: _____ Date: _____
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By: _____ Date: _____
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By: _____ Date: _____
Audrey Goddard

By: _____ Date: _____
Paul J. Godowski

By: _____ Date: 6/8/05
Austin L. Gurney

By: _____ Date: _____
James Pan

By: _____ Date: _____
Colin K. Watanabe

By: _____ Date: _____
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Audrey Goddard

By: _____ Date: _____
Paul J. Godowski

By: _____ Date: _____
Austin L. Gurney

By: _____ Date: June 9/05
James Pan

By: _____ Date: _____
Colin K. Watanabe

By: _____ Date: _____
William I. Wood

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By: _____ Date: _____
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By: _____ Date: _____
James Pan

By: _____ Date: _____
Colin K. Watanabe

By: William I. Wood Date: 5/27/05
William I. Wood

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EXHIBIT A

ASY92

Assay Name	Mouse Messengial Cell proliferation Assay
Alias Name	Mu Mess Cell Prolif
Status	Retired
Class	Primary
Format	96 Well
Type	Cell
Sample Requirements	
Assay Volume	0.1 ml
Fold Dil into Well	10 Fold
Replicates	3
Dilutions	2
Volume Requested	0.03ml/well/conc
Protocol	
Species	Mouse
Purpose	Screen SPDI proteins which can stimulate Messengial Cell Proliferation
Protocol	On day 1: Mouse messengial cells are plated on a 96 well plate in Media[A 3:1 mixture of Dulbecoo's modified Eagle's medium and Ham's F12 medium- 95%- fetal bovine serum-5%- supplemented with 14mM hepes] and grw overnight. On day 2: SPDI Proteins are diluted at 2 conc. [1%- 0.1%] in serum-free Media and added to the cells. On day 4: After 48 hours incubation- each well of the plate was added 20 µl of the Cell Titer 96 Aqueous one solution reagent [Promega] and colormetric reaction was allowed for 2 hours. The absorbance [OD] is measured at 490 nm.
Matrix	Promega kit for the assay-
Result Calculation	replicated average
Result Interpretation	Any PIN that gives an absorbance reading which is 15% above the media control is considered a hit.
Result Cutoff	> 15 %
	In Vivo: InVitro:
Comments	
Status	
Date Entered	
Date Canceled	
Department	Endocrinology
Scientist	James (Guohua) Pan
Notebook	0-
Assayers	

Status	Retired
Cancel Reason	
Bioarea	Endocrinology
Lab Scientist	Weiguang Mao

GenenGenes | SITEMAP | Additional Resources:

GENE VIEWER | GENE | FAM | MAP | GENEHUB
SEQUENCE VIEWER | DNA | SRC | RNA | LIB | FLS | OLI
ASSAY VIEWER | PRO | DOM | EXP | PUR | LOT | ASY

● Find ○ New ○ Update

SELECT | GO

[redacted]

Assay Viewer

SPDI Assays

ASY1 Heart Neonatal Hypertrophy
ASY2 Heart Adult Hypertrophy
ASY3 Adipocyte Lipolysis
ASY4 Adipocyte Lipogenesis
ASY5 Hematopoiesis: stem cell proliferation
ASY6 Hippocampal Neuron Survival
ASY7 Retinal Neuron Survival (5-6 days cultur
ASY8 Endothelial cell proliferation
ASY9 Inhibition of VEGF stimulated endothelia
ASY10 Eosinophil degranulation [induction of]
ASY11 B cell IgE synthesis inhibition

Select All | Unselect

Find Lots

All PIN
All DNA

Show Lots for: PIN
Number: 1205
☐ Include UNQ Related Lots

Clear

Lots for Search

PIN1205-1

Remove | Remove All

☑ All Positives ☐ Verified Positives ☐ Pending

Date Complete From ____ To ____

PUR Search | DNA Search | Reset

ASSAY RESULT LIST

Rows 1 - 2 of 2

Page 1 of 1

Select Page Page No. 1 GO

ASY	ASY Name	PUR/EXP/DNA	LOT	LOT Name	Pos	Verified	Conc	Conc Unit	Mean	Crtl	UNQ	Protein Name	Date Distr	Date Complete	Comment
ASY92	Mu.Mess Cell Prolif	PUR1715	LOT2447	PIN1205-1			0.10	%	1		UNQ1915	Human DPKL1915 IgG			
ASY92	Mu Mess Cell Prolif	PUR1715	LOT2447	PIN1205-1			1.00	%	1		UNQ1915	Human DPKL1915 IgG			

ASY | DNA | DOM | EXP | FAM | FLS | LIB | LOT | MAP | OLI | PRB | PRO | PUR | RNA | SRC | UNQ | XPT | YST
Assay Viewer | Sequence Viewer | Gene Viewer | GenenGenes | SAGE

GenenGenes Feedback

EXHIBIT B

>Thursday, April 28, 2005
>DNA92234 [Full]
>887 Sites [All Sites]
>   [DNA92234], sheldens
> Lib309
>Sequence confirmed by phredphrap

```
                                          thaI
                                      nlaIII     snaBI
                                     sphI   fnuDII/mvnI                  mnlI
                                     nspHI  bstUI taiI                 taqI
                                taiI nspI   bsh1236I                   xhoI
                                maeII/hpyCH4IV bsiWI/splI       tsp509I[M.ecoRI-]
                           aluI  hinlI/acyI cac8I   bsaAI        ecoRI    tliI
      tsp45I      sapI       ahaII/bsaHI  mluI rsaI       hpy188I     smlI
      maeIII      mboII      aatII  cac8I aflIII maeII/hpyCH4IV       paeR7I            hpy188I aciI       bpmI/g
    hphI   sfcI  earI/ksp632I hpy99I  hpyCH4V csp6I  aluI   apoI     avaI[M.taqI-]   mnlI     fnu4HI/bsoFI hpy18
1 TAGGTGACAC TATAGAAGAG CTATGACGTC GCATGCACGC GTACGTAAGC TCGGAATTCG GCTCGAGGAA TGAATACCTC CGAAGCCGCT TTGTTCTCCA
  ATCCACTGTG ATATCTTCTC GATACTGCAG CGTACGTGCG CATGCATTCG AGCCTTAAGC CGAGCTCCTT ACTTATGGAG GCTTCGGCGA AACAAGAGGT
                                                                    ^insert starts here
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                                                nciI
                                                mspI
                                                hpaII                                                   mnlI
                                                dsaV                                                    bslI
                                          bpuAI bssKI                    bsp1286                  tsp45I
                                          bbsI  bslI     bsmFI taiI      bmyI                tru9I  hphI
          aluI                      mnlI  mboII  bsaJI      maeII/hpyCH4IV                  mseI maeIII                nla
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                                                                                sau3AI
                                                                                mboI/ndeII[dam-]
                                                                                dpnII[dam-]
                                                                                dpnI[dam+]
                                                                                alwI[dam-]
                                                                              nlaIV
     pleI                                       mnlI                      bstYI/xhoII                hgaI
     mlyI                                   rmaI                          bamHI bslI              tseI
     hinfI                                  maeI      hpy188I bstXI       alwI[dam-]   hpy188III  fnu4HI/bso
   bsmFI  mnlI                mnlI           bfaI   eco57I   bpmI/gsuI[dcm-]   bslI  avaI        bbvI bsmFI
201 TGGGACTCCC TCTGCCACAT TTTTTGGAGG TTGGGAAAGT TGCTAGAGGC TTCAGAACTC CAGCCTAATG GATCCCAAAC TCGGGAGAAT GGCTGCGTCC
    ACCCTGAGGG AGACGGTGTA AAAAACCTCC AACCCTTTCA ACGATCTCCG AAGTCTTGAG GTCGGATTAC CTAGGGTTTG AGCCCTCTTA CCGACGCAGG
  1                                                                       M   D P K L   G R M   A A S
                                                                          ^MET
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                                                fnu4HI/bsoFI
                                        tseI    aciI
                                tseI    mwoI    thaI nlaIII                     haeII
                                mwoI    fnu4HI/bsoFI    nspHI                   mspI
                                fnu4HI/bsoFI    fnuDII/mvnI                     scrFI[M.hpaII-]
                                bbvI    bbvI    bstUI[M.hhaI-]                  nciI
                        tseI    tseI            bsh1236I                        dsaV hinPI          bpuAI                   ms
                        mwoI    fnu4HI/bsoFI hinPI nspI         hphI        mwoI hpaII              bbsI    rsaI    mnlI
            mwoI        fnu4HI/bsoFI        hhaI/cfoI       mnlI        aciI bssKI              xmnI mboII  csp6I   ecoNI
            cac8I       bbvI    bbvI    bpmI/gsuI[dcm-]     bseRI   mnlI bslI bsaJI hhaI/cfoI   asp700  bsrI    bslI
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    GACGACCGAC ACGACGACGA CGACGACCTC GCGCCGTACA AGAGGAGTGG GAGGGGCGGG GGCCGCGACA ATCTCTTTCA GAAGGTCATG TAACTGGAGG
 12 L  L  A  V   L  L  L   L  L  E   R  G  M  F   S  S  P   S  P  P   P  A  L  L   E  K  V   F  Q  Y   I  D  L  H

                                                                                                    mboII
                                                                                                    earI/ksp632I
                                                                                                    sapI
                                                                                                    aluI
                                                                                                    sstI
                                                                                                    sacI
                                                                        tth111I/aspI                hgiAI/aspHI[M.aluI-
                                                                        pleI                        ecl136II
                apoI        alwNI[dcm-]             haeIII/palI         pflFI                       bsp1286[M.aluI-]
            fokI tsp509I    alw26I/bsmAI            mscI/balI           mlyI                        bsiHKAI hpy188I
            bstF5I      hpyCH4V                     eaeI    taqI        hinfI                   hpy188I bmyI eco57I     ea
        hpy188III       bsgI hgaI eco57I            cfrI    hpy188III               mnlI    eco57I      banII[M.aluI-]  cf
401 ATCAGGATGA ATTTGTGCAG ACGCTGAAGG AGTGGGTGGC CATCGAGAGC GACTCTGTCC AGCCTGTGCC TCGCTTCAGA CAAGAGCTCT TCAGAATGAT
    TAGTCCTACT TAAACACGTC TGCGACTTCC TCACCCACCG GTAGCTCTCG CTGAGACAGG TCGGACACGG AGCGAAGTCT GTTCTCGAGA AGTCTTACTA
 46   Q  D  E   F  V  Q   T  L  K  E   W  V  A   I  E  S   D  S  V  Q   P  V  P   R  F  R   Q  E  L  F   R  M  M
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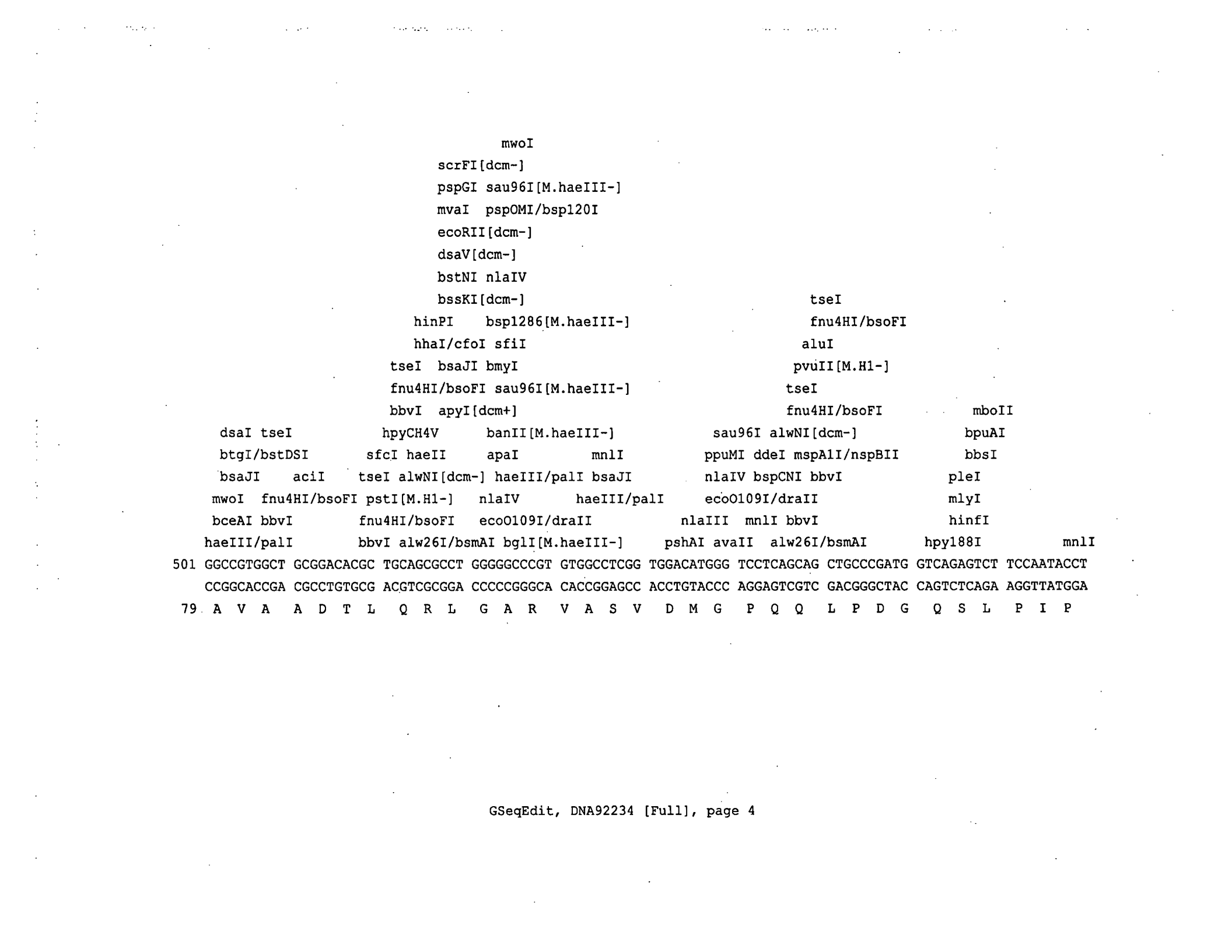
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scrFI[dcm-]
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mvaI pspOMI/bsp120I
ecoRII[dcm-]
dsaV[dcm-]
bstNI nlaIV
bssKI[dcm-]
hinPI bsp1286[M.haeIII-]
hhaI/cfoI sfiI
tseI bsaJI bmyI
fnu4HI/bsoFI sau96I[M.haeIII-]
bbvI apyI[dcm+]
tseI
fnu4HI/bsoFI
aluI
pvuII[M.H1-]
tseI
fnu4HI/bsoFI
mboII
dsaI tseI
hpyCH4V
banII[M.haeIII-]
sau96I alwNI[dcm-]
bpuAI
btgI/bstDSI
sfcI haeII
apaI
mnlI
ppuMI ddeI mspA1I/nspBII
bbsI
bsaJI
aciI
tseI alwNI[dcm-]
haeIII/palI bsaJI
nlaIV bspCNI bbvI
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mwoI
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nlaIV
haeIII/palI
eco0109I/draII
mlyI
bceAI bbvI
fnu4HI/bsoFI
eco0109I/draII
nlaIII mnlI bbvI
hinfI
haeIII/palI
bbvI alw26I/bsmAI bglI[M.haeIII-]
pshAI avaII alw26I/bsmAI
hpy188I
mnlI
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CCGGCACCGA CGCCTGTGCG ACGTCGCGGA CCCCCGGGCA CACCGGAGCC ACCTGTACCC AGGAGTCGTC GACGGGCTAC CAGTCTCAGA AGGTTATGGA
79 A V A A D T L Q R L G A R V A S V D M G P Q Q L P D G Q S L P I P

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       scrFI[dcm-]
       pspGI
       mvaI
       ecoRII[dcm-]                                                                               scrFI[M.hpaII-]
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       bssKI[dcm-]       mboI/ndeII[dam-] bst4CI/hpyCH4III            bsgI  cac8I     hpaII
       apyI[dcm+]        dpnII[dam-]    bstAPI          eaeI        taiI bbvI       dsaV
    fokI  cfrI   bsrI    dpnI[dam+]    nlaIV           cfrI        maeII/hpyCH4IV   bssKI
    bstF5I haeIII/palI   alwI[dam-]    banI      mwoI  bceAI      btrI hpyCH4V      bsaJI
601 CCCGTCATCC TGGCCGAACT GGGGAGCGAT CCCACGAAAG GCACCGTGTG CTTCTACGGC CACTTGGACG TGCAGCCTGC TGACCGGGGC GATGGGTGGC
    GGGCAGTAGG ACCGGCTTGA CCCCTCGCTA GGGTGCTTTC CGTGGCACAC GAAGATGCCG GTGAACCTGC ACGTCGGACG ACTGGCCCCG CTACCCACCG
112 P  V  I  L   A  E  L   G  S  D   P  T  K  G   T  V  C   F  Y  G   H  L  D  V   Q  P  A   D  R  G   D  G  W  L

                                                                                           sau3AI  mwoI
                                                                                 bslI      mboI/ndeII[dam-]
    sau96I                                                                   sau96I[M.haeIII-] dpnII[dam-]   hi
    nlaIV                 accI                   mnlI   mcrI                 haeIII/palI       dpnI[dam+]    hh
    avaII              mnlI                      bseRI  bsiEI              eco0109I/draII     alwI[dam-]    hae
701 TCACGGACCC CTATGTGCTG ACGGAGGTAG ACGGGAAACT TTATGGACGA GGAGCGACCG ACAACAAAGG CCCTGTCTTG GCTTGGATCA ATGCTGTGAG
    AGTGCCTGGG GATACACGAC TGCCTCCATC TGCCCTTTGA AATACCTGCT CCTCGCTGGC TGTTGTTTCC GGGACAGAAC CGAACCTAGT TACGACACTC
146  T  D  P   Y  V  L   T  E  V  D   G  K  L   Y  G  R   G  A  T  D   N  K  G   P  V  L   A  W  I  N   A  V  S
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                  scrFI[dcm-]                                                                    mnlI
                  pspGI                                                                         bpmI/gsuI[dcm-]
                  mvaI        sau3AI                                                            scrFI[dcm-]
                  ecoRII[dcm-]                                                                  pspGI
                  dsaV[dcm-] mboI/ndeII[dam-]                                                   mvaI
                  bstNI       dpnII[dam-]                                                       ecoRII[dcm-]
               bsp1286        bstYI/xhoII                                                       dsaV[dcm-]
               bmyI bssKI[dcm-]  mboII                                                          bstNI
            hpy188I apyI[dcm+] dpnI[dam+]                              fokI  mboII cac8I       bssKI[dcm-]
          eco57I   bsaJI       bglII                 tsp509I         bstF5I   mnlI            apyI[dcm+]
        mwoI   banII bpmI/gsuI[dcm-]                 apoI         mnlI      earI/ksp632I        bsaJI
801 CGCCTTCAGA GCCCTGGAGC AAGATCTTCC TGTGAATATC AAATTCATCA TTGAGGGGAT GGAAGAGGCT GGCTCTGTTG CCCTGGAGGA ACTTGTGGAA
    GCGGAAGTCT CGGGACCTCG TTCTAGAAGG ACACTTATAG TTTAAGTAGT AACTCCCCTA CCTTCTCCGA CCGAGACAAC GGGACCTCCT TGAACACCTT
179  A  F  R   A  L  E  Q   D  L  P   V  N  I   K  F  I  I   E  G  M   E  E  A   G  S  V  A   L  E  E   L  V  E
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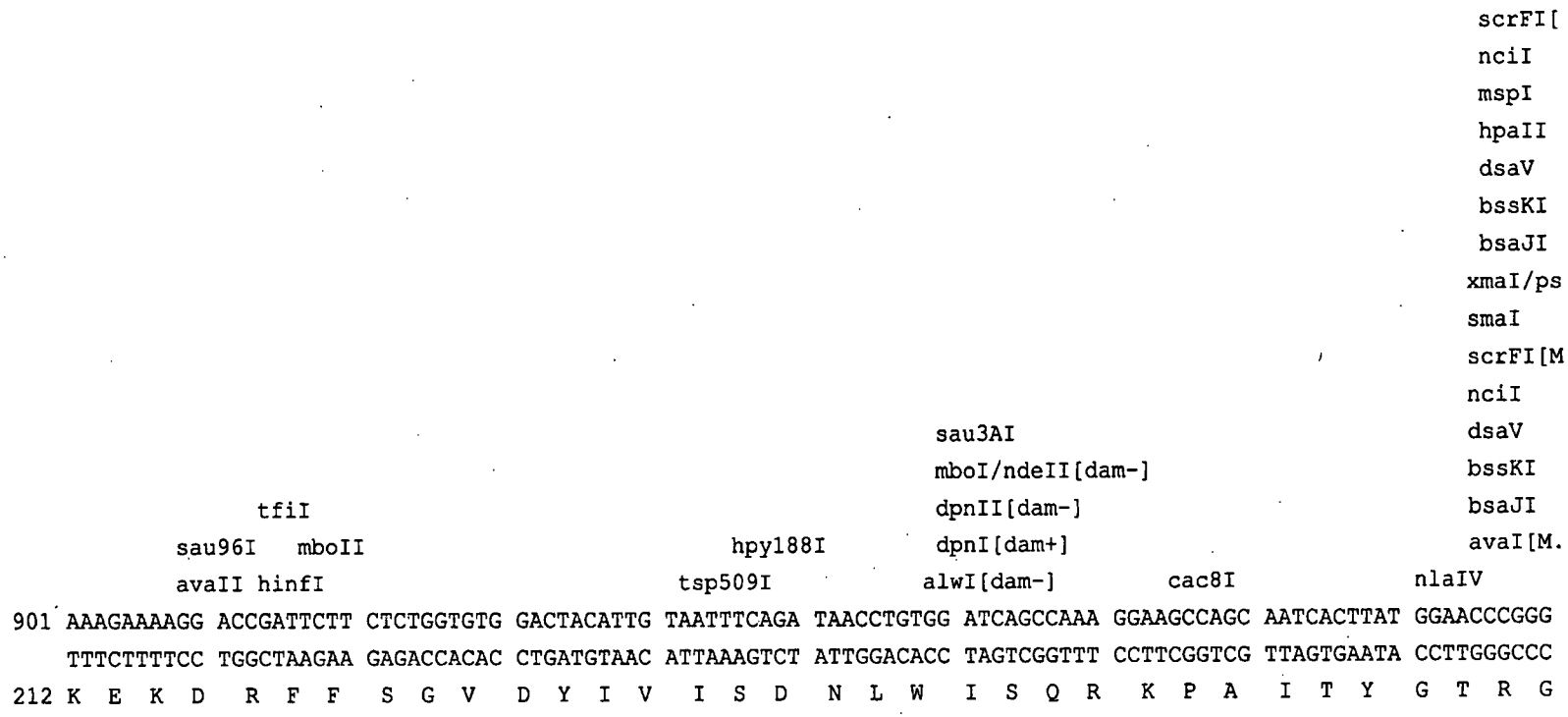
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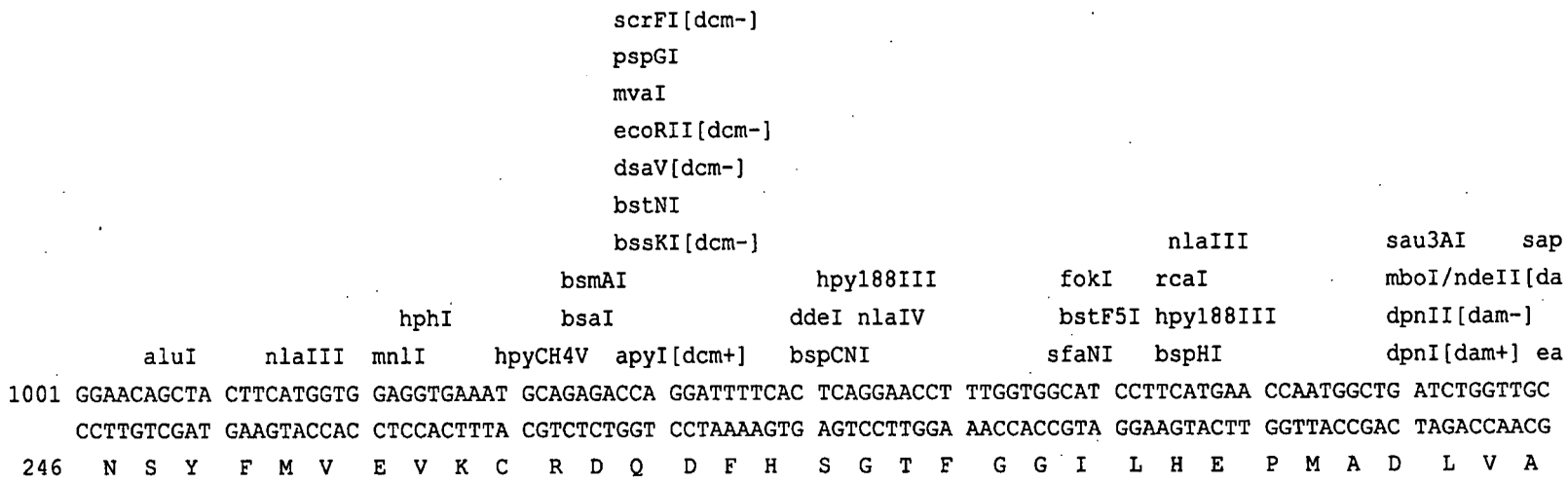
hpaII
dsaV
bssKI
bsaJI
xmaI/ps
smaI
scrFI[M
nciI
sau3AI
dsaV
mboI/ndeII[dam-]
bssKI
tfiI
dpnII[dam-]
bsaJI
sau96I mboII
hpy188I
dpnI[dam+]
avaI[M.
avaII hinfI
tsp509I
alwI[dam-]
cac8I
nlaIV
901 AAAGAAAAGG ACCGATTCTT CTCTGGTGTG GACTACATTG TAATTTCAGA TAACCTGTGG ATCAGCCAAA GGAAGCCAGC AATCACTTAT GGAACCCGGG
TTTCTTTTCC TGGCTAAGAA GAGACCACAC CTGATGTAAC ATTAAAGTCT ATTGGACACC TAGTCGGTTT CCTTCGGTCG TTAGTGAATA CCTTGGGCCC
212 K E K D R F F S G V D Y I V I S D N L W I S Q R K P A I T Y G T R G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ecoRII[dcm-]
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bstNI
bssKI[dcm-]
nlaIII
sau3AI
sap
bsmAI
hpy188III
fokI
rcaI
mboI/ndeII[da
hphI
bsaI
ddeI nlaIV
bstF5I
hpy188III
dpnII[dam-]
aluI
nlaIII
mnlI
hpyCH4V
apyI[dcm+]
bspCNI
sfaNI
bspHI
dpnI[dam+] ea
1001 GGAACAGCTA CTTCATGGTG GAGGTGAAAT GCAGAGACCA GGATTTTCAC TCAGGAACCT TTGGTGGCAT CCTTCATGAA CCAATGGCTG ATCTGGTTGC
CCTTGTCGAT GAAGTACCAC CTCCACTTTA CGTCTCTGGT CCTAAAAGTG AGTCCTTGGA AACCACCGTA GGAAGTACTT GGTTACCGAC TAGACCAACG
246 N S Y F M V E V K C R D Q D F H S G T F G G I L H E P M A D L V A

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                                                    scrFI[dcm-]
                                                    pspGI
                                                    mvaI
                                                    ecoRII[dcm-]
                                                    dsaV[dcm-]
                                                    bstNI
                                                    bssKI[dcm-]
                                                sau96I[dcm-]
                                                nlaIV
                    accI                        avaII[dcm-]
                scrFI[dcm-]                 scrFI[dcm-]
                pspGI  pleI                 pspGI   apyI[dcm+]
                mvaI   mlyI                 mvaI bsmFI
                ecoRII[dcm-]                ecoRII[dcm-]
                dsaV[dcm-]                  dsaV[dcm-]
                bstNI  hinfI                bstNI  bsaJI                                    mnlI
                bssKI[dcm-]                 bssKI[dcm-] tfiI        xmnI  nlaIV         mboII
    mboII       apyI[dcm+]                  apyI[dcm+]  hinfI       asp700    mnlI      earI/ksp632I
1101 TCTTCTCGGT AGCCTGGTAG ACTCGTCTGG TCATATCCTG GTCCCTGGAA TCTATGATGA AGTGGTTCCT CTTACAGAAG AGGAAATAAA TACATACAAA
     AGAAGAGCCA TCGGACCATC TGAGCAGACC AGTATAGGAC CAGGGACCTT AGATACTACT TCACCAAGGA GAATGTCTTC TCCTTTATTT ATGTATGTTT
 279  L  L  G   S  L  V  D   S  S  G   H  I  L   V  P  G  I   Y  D  E   V  V  P   L  T  E  E   E  I  N   T  Y  K
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                                             scrFI[M.hpaII-]                                                          rsaI
                                             nciI                                                                     csp6I
                                             mspI                                                                     nlaIV
                                             hpaII                                                                    kpnI
            rmaI                             dsaV                                                                     banI
            maeI    rmaI                     bssKI                                                                    asp718
           xbaI     maeI        mspI     tseI                                                                  bpmI/gsuI[dcm
     fokI  hpy188III  mboII     hpaII    fnu4HI/bsoFI   tsp509I                mnlI  tfiI          mnlI      hpy188III
     bstF5I bfaI    bfaI       bsaWI     bbvI          apoI          taqI   ddeI bseRI hinfI    hpyCH4V    mnlI      acc65I
1201 GCCATCCATC TAGACCTAGA AGAATACCGG AATAGCAGCC GGGTTGAGAA ATTTCTGTTC GATACTAAGG AGGAGATTCT AATGCACCTC TGGAGGTACC
     CGGTAGGTAG ATCTGGATCT TCTTATGGCC TTATCGTCGG CCCAACTCTT TAAAGACAAG CTATGATTCC TCCTCTAAGA TTACGTGGAG ACCTCCATGG
312 A  I  H  L   D  L  E   E  Y  R   N  S  S  R   V  E  K   F  L  F   D  T  K  E   E  I  L   M  H  L   W  R  Y  P

                                                                         haeIII/palI
                                                                        eaeI[dcm-]
                             thaI                                       cfrI
                             fnuDII/mvnI    scrFI[dcm-]                scrFI[dcm-]
                            hinPI           pspGI                      pspGI
                        mnlI bstUI[M.hhaI-] mvaI                       mvaI
                   sau3AI   hhaI/cfoI       ecoRII[dcm-]               ecoRII[dcm-]
                   mboI/ndeII[dam-][M.taqI-]                           dsaV[dcm-]
                   dpnII[dam-]              dsaV[dcm-]                 bstNI              tsp509I         bsm
                   dpnI[dam+]               bstNI                      bssKI[dcm-]       apoI           rmaI
                  alwI[dam-] bsh1236I       bssKI[dcm-]                apyI[dcm+]      xmnI             maeI
              nlaIII  taqI[dam-]            apyI[dcm+]  bst4CI/hpyCH4III               asp700           bfaI
1301 CATCTCTTTC TATTCATGGG ATCGAGGGCG CGTTTGATGA GCCTGGAACT AAAACAGTCA TACCTGGCCG AGTTATAGGA AAATTTTCAA TCCGTCTAGT
     GTAGAGAAAG ATAAGTACCC TAGCTCCCGC GCAAACTACT CGGACCTTGA TTTTGTCAGT ATGGACCGGC TCAATATCCT TTTAAAAGTT AGGCAGATCA
346   S  L  S   I  H  G   I  E  G  A   F  D  E   P  G  T   K  T  V  I   P  G  R   V  I  G   K  F  S  I   R  L  V
```

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                                                                                                                                   pl
        nlaIII                        tsp45I                                                                                       ml
      mslI                            maeIII           mboII                 xmnI                                                  hi
   mnlI mslI            aciI         hphI          hpy188III                 asp700     bstXI                                   nlaII
1401 CCCTCACATG AATGTGTCTG CGGTGGAAAA ACAGGTGACA CGACATCTTG AAGATGTGTT CTCCAAAAGA AATAGTTCCA ACAAGATGGT TGTTTCCATG
     GGGAGTGTAC TTACACAGAC GCCACCTTTT TGTCCACTGT GCTGTAGAAC TTCTACACAA GAGGTTTTCT TTATCAAGGT TGTTCTACCA ACAAAGGTAC
 379 P  H  M   N  V  S  A   V  E  K   Q  V  T   R  H  L  E   D  V  F   S  K  R   N  S  S  N   K  M  V   V  S  M

                                                                                            tspRI
                                                                                     hpy188I                               sau
                                                                       mwoI        sau3AI  bst4CI/hpyCH4III                mbo
     rmaI         dsaI                                                tseI         mboI/ndeII[dam-]                        dpn
     maeI         btgI/bstDSI  sspI                                   fnu4HI/bsoFI dpnII[dam-]                             dpn
     bfaI         bsaJI     hpyCH4V                 bsrI              bbvI         dpnI[dam+]                              alw
1501 ACTCTAGGAC TACACCCGTG GATTGCAAAT ATTGATGACA CCCAGTATCT CGCAGCAAAA AGAGCGATCA GAACAGTGTT TGGAACAGAA CCAGATATGA
     TGAGATCCTG ATGTGGGCAC CTAACGTTTA TAACTACTGT GGGTCATAGA GCGTCGTTTT TCTCGCTAGT CTTGTCACAA ACCTTGTCTT GGTCTATACT
 412 T  L  G  L   H  P  W   I  A  N   I  D  D  T   Q  Y  L   A  A  K   R  A  I  R   T  V  F   G  T  E   P  D  M  I
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              sau3AI
              mboI/ndeII[dam-]
              dpnII[dam-]                              sau3AI
          fokI dpnI[dam+]                       scrFI[dcm-]
          bstF5I                                pspGI  mboI/ndeII[dam-]
       scrFI[M.hpaII-]                          mvaI   dpnII[dam-]
       nciI   alwI[dam-]                        ecoRII[dcm-]
       mspI   nlaIV                             dsaV[dcm-]
       hpaII  bstYI/xhoII                       bstNI  dpnI[dam+]                     mspA1I/nspBII
       dsaV   bamHI           tsp509I           bssKI[dcm-]                       tsp509I
       bssKI  alwI[dam-]     munI/mfeI          apyI[dcm+]                     mwoI    aciI    aluI
1601 TCCGGGATGG ATCCACCATT CCAATTGCCA AAATGTTCCA GGAGATCGTC CACAAGAGCG TGGTGCTAAT TCCGCTGGGA GCTGTTGATG ATGGAGAACA
     AGGCCCTACC TAGGTGGTAA GGTTAACGGT TTTACAAGGT CCTCTAGCAG GTGTTCTCGC ACCACGATTA AGGCGACCCT CGACAACTAC TACCTCTTGT
446   R  D  G   S  T  I   P  I  A  K   M  F  Q   E  I  V   H  K  S  V   V  L  I   P  L  G   A  V  D  D   G  E  H

                                                                                                        tru9I
                                                                    tseI                      aluI    mseI
                                                      nlaIV         fnu4HI/bsoFI            sau96I[M.haeIII-]
                                                  mnlI        tsp509I  bbvI        ddeI     haeIII/palI aseI/asnI/vspI
1701 TTCGCAGAAT GAGAAAATCA ACAGGTGGAA CTACATAGAG GGAACCAAAT TATTTGCTGC CTTTTTCTTA GAGATGGCCC AGCTCCATTA ATCACAAGAA
     AAGCGTCTTA CTCTTTTAGT TGTCCACCTT GATGTATCTC CCTTGGTTTA ATAAACGACG GAAAAAGAAT CTCTACCGGG TCGAGGTAAT TAGTGTTCTT
479  S  Q  N   E  K  I  N   R  W  N   Y  I  E   G  T  K  L   F  A  A   F  F  L   E  M  A  Q   L  H  O
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                    sau3AI
                    mboI/ndeII[dam-]
                    dpnII[dam-]
                    dpnI[dam+]
                 hpy188I                              rmaI
               sau3AI    tspRI                        maeI
            hpy188I  alwI[dam-]                      bslI
         rmaI    mboI/ndeII[dam-]      hphI          bslI                              tsp509I   rmaI
         maeI    dpnII[dam-]       tfiI   mnlI      fokI bfaI     fokI                  apoI      maeI     rsaI
         bfaI    dpnI[dam+]        hinfI[M.hphI-]   bstF5I        bstF5I          hpy188III       bfaI     csp6I
1801 CCTTCTAGTC TGATCTGATC CACTGACAGA TTCACCTCCC CCACATCCCT AGACAGGGAT GGAATGTAAA TATCCAGAGA ATTTGGGTCT AGTATAGTAC
     GGAAGATCAG ACTAGACTAG GTGACTGTCT AAGTGGAGGG GGTGTAGGGA TCTGTCCCTA CCTTACATTT ATAGGTCTCT TAAACCCAGA TCATATCATG

                                                                                          sau96I
                                    sau3AI                                                nlaIV
                                    mboI/ndeII[dam-]                                      avaII      hpyCH4V
                                    dpnII[dam-]                                          ppuMI      bsgI
                  tru9I             dpnI[dam+]                                           eco0109I/draII
                  mseI           hpy188III                                            tru9I       tspRI
                 ahaIII/draI   ecoRV   alwI[dam-]    sspI                             mseI bsmFI  btsI
1901 ATTTTCCCTT CCATTTAAAA TGTCTTGGGA TATCTGGATC AGTAATAAAA TATTTCAAAG GCACAGATGT TGGAAATGGT TTAAGGTCCC CCACTGCACA
     TAAAAGGGAA GGTAAATTTT ACAGAACCCT ATAGACCTAG TCATTATTTT ATAAAGTTTC CGTGTCTACA ACCTTTACCA AATTCCAGGG GGTGACGTGT
```

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                                                                              scrFI[dcm-]
                                                                              pspGI
                                                                              mvaI
                                                                              ecoRII[dcm-]
                          tseI                                                dsaV[dcm-]
                      cac8I                                                   bstNI
                   tseI   fnu4HI/bsoFI                                        bssKI[dcm-]
                   fnu4HI/bsoFI                                               apyI[dcm+]
        smlI       bbvI   bbvI                                              bslI      tfiI
       mnlI       aluI   hpyCH4V                                    hpyCH4V bsaJI     hinfI
2001 CCTTCCTCAA GTCATAGCTG CTTGCAGCAA CTTGATTTCC CCAAGTCCTG TGCAATAGCC CCAGGATTGG ATTCCTTCCA ACCTTTTAGC ATATCTCCAA
     GGAAGGAGTT CAGTATCGAC GAACGTCGTT GAACTAAAGG GGTTCAGGAC ACGTTATCGG GGTCCTAACC TAAGGAAGGT TGGAAAATCG TATAGAGGTT

                                                  sau96I         tsp45I
                                                  avaII       bssSI
                                                 ppuMI       hgiAI/aspHI
                                                 eco0109I/draII hpy188III                       sau3AI
                              mspI         rmaI          bsp1286                                mboI/ndeII[dam-]
         tsp509I              hpaII        maeI    smlI  bsiHKAI                         fokI   dpnII[dam-]
      hpyCH4V                bsaWI         bfaI   mnlI   bmyI   maeIII                   bstF5I dpnI[dam+]
2101 CCTTGCAATT TGATTGGCAT AATCACTCCG GTTTGCTTTC TAGGTCCTCA AGTGCTCGTG ACACATAATC ATTCCATCCA ATGATCGCCT TTGCTTTACC
     GGAACGTTAA ACTAACCGTA TTAGTGAGGC CAAACGAAAG ATCCAGGAGT TCACGAGCAC TGTGTATTAG TAAGGTAGGT TACTAGCGGA AACGAAATGG

                     tru9I
                     mseI             bsmAI
                    aseI/asnI/vspI   bsaI      tspRI
2201 ACTCTTTCCT TTTATCTTAT TAATAAAAAT GTTGGTCTCC ACCACTGNCT CCCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
     TGAGAAAGGA AAATAGAATA ATTATTTTTA CAACCAGAGG TGGTGACNGA GGGTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT
```

```
                                                  scrFI[M.hpaII-]
                                                  nciI
                                                  mspI
                                                  hpaII
                                                  dsaV
                                                  bssKI           sau96I rsaI
                                                 xmaI/pspAI      rsrII/cspI
                                                  smaI          mroI     nlaIV
                                    aciI          scrFI[M.hpaII-] cpoI   kpnI  hpyCH4V
                                   fnu4HI/bsoFI          taqI nciI          hpy188III csp6I
                                   haeIII/palI     sstI  salI  dsaV          bspMII   banI sfcI
                                  mcrI             sacI  hincII/hindII[M.taqI-] avaII[M.hpaII-]
                                  eagI/xmaIII/eclXI aluI accI[M.taqI-]  tru9I mspI    asp718
                                  eaeI             hgiAI/aspHI[M.aluI-] mseI bspEI cfr10I/bsrFI
                                  cfrI       rmaI  ecl136II    bssKI  aseI/asnI/vspI  acc65I  cac8I
                                  bsiEI      maeI  bsp1286[M.aluI-] xmnI  tsp509I  bsaWI   pstI
                                 notI        bfaI  bsiHKAI     bsaJI tsp509I bsaWI ageI   sse8387I
                                 fnu4HI/bsoFI      bmyI hpy99I avaI[M.hpaII-] hpaII mspI bspMI      rsaI
                                 aciI       speI   banII[M.aluI-]   asp700   accIII hpaII sbfI      csp6I aluI    sf
2301 AAAAAAAAAA AAAAAAAAAA AAAGGGCGGC CGCCGACTAG TGAGCTCGTC GACCCGGGAA TTAATTCCGG ACCGGTACCT GCAGGCGTAC CAGCTTTCCC
     TTTTTTTTTT TTTTTTTTTT TTTCCCGCCG GCGGCTGATC ACTCGAGCAG CTGGGCCCTT AATTAAGGCC TGGCCATGGA CGTCCGCATG GTCGAAAGGG

           pleI
           mlyI
           hinfI        aluI
2401 TATAGTGAGT CGTATTAGAG CTTGG
     ATATCACTCA GCATAATCTC GAACC
```

> length: 2425

aatII(GACGTC): 25
acc65I(GGTACC): 1295 2374
accI(GTMKAC): 727 1117 2348
accIII(TCCGGA): 2366
aciI(CCGC): 86 332 355 511 1420 1672 2326 2330
acyI(GRCGYC): 25
aflIII(ACRYGT): 37
ageI(ACCGGT): 2371
ahaII(GRCGYC): 25
ahaIII(TTTAAA): 1914
aluI(AGCT): 19 48 110 485 569 1006 1680 1781 2016 2343 2392 2419
alw26I(CAGNNNCTG): 418 523 565
alwI(GGATCNNNN): 270 271 628 785 959 1319 1599 1609 1610 1817 1936
alwNI(CAGNNNCTG): 418 523 565
apaI(GGGCCC): 533
apoI(RAATTY): 54 409 841 1249 1381 1879
apyI(CCWGG): 528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
aseI(ATTAAT): 1787 2219 2360
asnI(ATTAAT): 1787 2219 2360
asp700(GAANNNNTTC): 375 1159 1379 1469 2358
asp718(GGTACC): 1295 2374
aspHI(GWGCWC): 484 2152 2342
aspI(GACNNNGTC): 451
avaI(CYCGRG): 62 280 995 2353
avaII(GGWCC): 559 705 909 1140 1985 2143 2369
balI(TGGCCA): 437
bamHI(GGATCC): 270 1609
banI(GGYRCC): 640 1295 2374

banII(GRGCYC): 484 533 809 2342
bbsI(GAAGACNNNNNN): 130 379 587
bbvI(GCAGC): 292 312 315 318 321 508 519 522 567 570 672 1235 1552 1756 2017 2024
bceAI(ACGGCNNNNNNNNNNNN): 502 656
bfaI(CTAG): 243 1210 1216 1396 1504 1805 1849 1889 2140 2337
bglI(GCCNNNNNGGC): 535
bglII(AGATCT): 822
bmyI(GDGCHC): 159 484 533 809 2152 2342
bpmI(CTGGAG): 96 258 325 814 883 1290
bpuAI(GAAGACNNNNNNN): 130 379 587
bsaAI(YACGTR): 42
bsaHI(GRCGYC): 25
bsaI(GGTCTCNNNNN): 1034 2234
bsaJI(CCNNGG): 139 359 503 528 545 684 812 881 995 996 1143 1516 2060 2353
bsaWI(WCCGGW): 1226 2127 2366 2371
bseRI(GAGGAGNNNNNNNNNN): 342 749 1270
bsgI(GTGCAG): 415 670 1994
bsh1236I(CGCG): 38 331 1329
bsiEI(CGRYCG): 755 2327
bsiHKAI(GWGCWC): 484 2152 2342
bsiWI(CGTACG): 40
bslI(CCNNNNNNNGG): 135 184 274 275 354 396 614 631 771 1847 1848 2060
bsmAI(GTCTC): 1034 2235
bsmAI(GTCTC): 1034 2235
bsmFI(GGGACNNNNNNNNNNNNNN): 143 202 297 1141 1399 1986
bsoFI(GCNGC): 85 292 312 315 318 321 332 508 519 522 567 570 672 1235 1552 1756 2017 2024 2326 2329
bsp120I(GGGCCC): 533
bsp1286(GDGCHC): 159 484 533 809 2152 2342
bspCNI(CTCAGNNNNNNNNN): 563 1050

bspEI(TCCGGA): 2366
bspHI(TCATGA): 1074
bspMI(ACCTGC): 2377
bspMII(TCCGGA): 2366
bsrFI(RCCGGY): 2371
bsrI(ACTGGN): 384 618 1542
bssKI(CCNGG): 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342 1363 1602 1638 2061 2353 2354
bssSI(CTCGTG): 2155
bst4CI(ACNGT): 643 1354 1573
bstAPI(GCANNNNNTGC): 641
bstDSI(CCRYGG): 503 1516
bstF5I(GGATG): 405 606 857 1068 1203 1605 1844 1857 2175
bstNI(CCWGG): 528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
bstUI(CGCG): 38 331 1329
bstXI(CCANNNNNNTGG): 260 1478
bstYI(RGATCY): 270 822 1609
btgI(CCRYGG): 503 1516
btrI(CACGTC): 667
btsI(GCAGTGNN): 1992
cac8I(GCNNGC): 31 35 303 675 868 975 2020 2381
cfoI(GCGC): 330 364 525 800 1328
cfr10I(RCCGGY): 2371
cfrI(YGGCCR): 437 500 611 657 1365 2327
cpoI(CGGWCCG): 2368
csp6I(GTAC): 41 387 1296 1897 2375 2387
cspI(CGGWCCG): 2368
ddeI(CTNAG): 563 1050 1265 1767
dpnI(GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937 2183

dpnII(GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937 2183

draI(TTTAAA): 1914

draII(RGGNCCY): 532 558 768 1984 2142

draIII(CACNNNGTG): 642

dsaI(CCRYGG): 503 1516

dsaV(CCNGG): 139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342 1363 1602 1638 2061 2353 2354

eaeI(YGGCCR): 437 500 611 657 1365 2327

eagI(CGGCCG): 2327

earI(CTCTTCNNNN): 15 487 862 1100 1177

ecl136II(GAGCTC): 484 2342

eclXI(CGGCCG): 2327

eco57I(CTGAAG): 250 424 474 489 804

ecoNI(CCTNNNNNAGG): 396

ecoO109I(RGGNCCY): 532 558 768 1984 2142

ecoRI(GAATTC): 54

ecoRII(CCWGG): 528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061

ecoRV(GATATC): 1929

fnu4HI(GCNGC): 85 292 312 315 318 321 332 508 519 522 567 570 672 1235 1552 1756 2017 2024 2326 2329

fnuDII(CGCG): 38 331 1329

fokI(GGATG): 405 606 857 1068 1203 1605 1844 1857 2175

gsuI(CTGGAG): 96 258 325 814 883 1290

haeII(RGCGCY): 363 524 799

haeIII(GGCC): 438 501 534 543 612 658 769 1366 1776 2328

hgaI(GACGC): 295 420

hgiAI(GWGCWC): 484 2152 2342

hhaI(GCGC): 330 364 525 800 1328

hinPI(GCGC): 330 364 525 800 1328

hincII(GTYRAC): 2348
hindII(GTYRAC): 2348
hinfI(GANTC): 204 451 585 914 1120 1148 1275 1500 1829 2070 2407
hinlI(GRCGYC): 25
hpaII(CCGG): 139 361 684 996 1227 1239 1602 2128 2354 2367 2372
hphI(GGTGA): 3 181 346 1023 1434 1832
hpy188I(TCNGA): 51 79 252 476 491 582 806 946 1568 1809 1814
hpy188III(TCNNGA): 97 281 402 443 1051 1074 1209 1289 1446 1873 1933 2156 2366
hpy99I(CGWCG): 27 2347
hpyCH4III(ACNGT): 643 1354 1573
hpyCH4IV(ACGT): 26 43 149 668
hpyCH4V(TGCA): 34 416 521 671 1030 1283 1524 1995 2023 2051 2104 2380
kpnI(GGTACC): 1295 2374
ksp632I(CTCTTCNNNN): 15 487 862 1100 1177
maeI(CTAG): 243 1210 1216 1396 1504 1805 1849 1889 2140 2337
maeII(ACGT): 26 43 149 668
maeIII(GTNAC): 4 180 1435 2158
mboI(GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937 2183
mboII(GAAGA): 15 131 380 488 588 825 862 917 1101 1177 1219 1450
mcrI(CGRYCG): 755 2327
mfeI(CAATTG): 1622
mluI(ACGCGT): 37
mlyI(GAGTCNNNNN): 204 451 585 1120 1500 2407
mnlI(CCTC): 65 77 126 185 209 227 246 344 350 396 469 545 562 598 724 749 853 865 886 1021 1168 1180 1270 1287 1293 1324 1402 1738 1835 2005 2146
mroI(TCCGGA): 2366
mscI(TGGCCA): 437
mseI(TTAA): 175 1788 1915 1981 2220 2361
mslI(CAYNNNNRTG): 400 1405 1407

mspA1I(CMGCKG): 568 1672
mspI(CCGG): 139 361 684 996 1227 1239 1602 2128 2354 2367 2372
munI(CAATTG): 1622
mvaI(CCWGG): 528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
mvnI(CGCG): 38 331 1329
mwoI(GCNNNNNNNGC): 303 312 315 321 357 502 535 641 650 793 802 1555 1665
nciI(CCSGG): 139 360 684 995 996 1239 1602 2353 2354
ndeII(GATC): 271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937 2183

nlaIII(CATG): 32 199 336 555 1014 1075 1315 1407 1497
nlaIV(GGNNCC): 270 532 533 558 640 705 991 1054 1140 1164 1295 1609 1741 1985 2374
notI(GCGGCCGC): 2326
nspBII(CMGCKG): 568 1672
nspHI(RCATGY): 31 335
nspI(RCATGY): 31 335
paeR7I(CTCGAG): 62
palI(GGCC): 438 501 534 543 612 658 769 1366 1776 2328
pflFI(GACNNNGTC): 451
pleI(GAGTCNNNN): 204 451 585 1120 1500 2407
ppuMI(RGGWCCY): 558 1984 2142
pshAI(GACNNNNGTC): 553
pspAI(CCCGGG): 995 2353
pspGI(CCWGG): 528 609 813 882 1038 1113 1137 1144 1342 1363 1638 2061
pspOMI(GGGCCC): 533
pstI(CTGCAG): 520 2379
pvuII(CAGCTG): 568
rcaI(TCATGA): 1074
rmaI(CTAG): 243 1210 1216 1396 1504 1805 1849 1889 2140 2337
rsaI(GTAC): 41 387 1296 1897 2375 2387
rsrII(CGGWCCG): 2368

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sacI(GAGCTC):                    484 2342
salI(GTCGAC):                    2348
sapI(GCTCTTCNNNN):               15 486 1099
sau3AI(GATC):                    271 628 786 823 960 1090 1320 1566 1599 1610 1644 1812 1817 1937
                                 2183
sau96I(GGNCC):                   533 534 559 705 769 909 1140 1776 1985 2143 2369
sbfI(CCTGCAGG):                  2378
scrFI(CCNGG):                    139 360 528 609 684 813 882 995 996 1038 1113 1137 1144 1239 1342
                                 1363 1602 1638 2061 2353 2354
sfaNI(GCATC):                    1067
sfcI(CTRYAG):                    10 520 2379 2400
sfiI(GGCCNNNNNGGCC):             534
smaI(CCCGGG):                    995 2353
smlI(CTYRAG):                    62 2006 2147
snaBI(TACGTA):                   42
speI(ACTAGT):                    2336
sphI(GCATGC):                    31
splI(CGTACG):                    40
sse8387I(CCTGCAGG):              2378
sspI(AATATT):                    1528 1949
sstI(GAGCTC):                    484 2342
taiI(ACGT):                      26 43 149 668
taqI(TCGA):                      63 443 1259 1322 2349
tfiI(GAWTC):                     914 1148 1275 1829 2070
thaI(CGCG):                      38 331 1329
tliI(CTCGAG):                    62
tru9I(TTAA):                     175 1788 1915 1981 2220 2361
tseI(GCWGC):                     292 312 315 318 321 508 519 522 567 570 672 1235 1552 1756 2017 2024
tsp45I(GTSAC):                   4 180 1435 2158
tsp509I(AATT):                   55 410 842 942 1250 1382 1623 1668 1748 1880 2107 2359 2363
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tspRI(NNCAGTGNN): 1574 1821 1992 2243
tth111I(GACNNNGTC): 451
vspI(ATTAAT): 1787 2219 2360
xbaI(TCTAGA): 1209
xhoI(CTCGAG): 62
xhoII(RGATCY): 270 822 1609
xmaI(CCCGGG): 995 2353
xmaIII(CGGCCG): 2327
xmnI(GAANNNNTTC): 375 1159 1379 1469 2358

not found:
aclI(AACGTT),afeI(AGCGCT),aflII(CTTAAG),ahdI(GACNNNNNGTC),alw44I(GTGCAC),apaLI(GTGCAC),ascI(GGCGCGCC),
avaIII(ATGCAT),aviII(TGCGCA),avrII(CCTAGG),baeI(NNNNNNNNNNNNNNNACNNNNGTAYCNNNNNNNNNNNN),bbrPI(CACGTG),
bcgI(NNNNNNNNNNNNCGANNNNNNNTGCNNNNNNNNNNNN),bciVI(GTATCC),bclI(TGATCA),bfrBI(ATGCAT),bfrI(CTTAAG),blnI(CCTAGG),
blpI(GCTNAGC),bpu1102I(GCTNAGC),bsaBI(GATNNNNATC),bsaXI(NNNNNNNNNNNNACNNNNNCTCCNNNNNNNNNN),bsiCI(TTCGAA),
bsmBI(CGTCTCNNNNN),bsmI(GAATGCN),bsp106(ATCGAT),bsp1407I(TGTACA),bspCI(CGATCG),bspDI(ATCGAT),bsrBI(GAGCGG),
bsrDI(GCAATGNN),bsrGI(TGTACA),bssHII(GCGCGC),bst1107I(GTATAC),bstBI(TTCGAA),bstEII(GGTNACC),bstZ17I(GTATAC),
bsu36I(CCTNAGG),celII(GCTNAGC),claI(ATCGAT),drdI(GACNNNNNNGTC),eam1105I(GACNNNNNGTC),eciI(GGCGGA),eco47III(AGCGCT),
eco72I(CACGTG),eco81I(CCTNAGG),eheI(GGCGCC),esp3I(CGTCTC),espI(GCTNAGC),fseI(GGCCGGCC),fspI(TGCGCA),hindIII(AAGCTT),
hpaI(GTTAAC),kasI(GGCGCC),kspI(CCGCGG),mamI(GATNNNNATC),mstII(CCTNAGG),naeI(GCCGGC),narI(GGCGCC),ncoI(CCATGG),
ndeI(CATATG),ngoMI(GCCGGC),nheI(GCTAGC),nruI(TCGCGA),nsiI(ATGCAT),pacI(TTAATTAA),pciI(ACATGT),pflMI(CCANNNNNTGG),
pmeI(GTTTAAAC),pmlI(CACGTG),ppu10I(ATGCAT),psiI(TTATAA),psp1406I(AACGTT),pvuI(CGATCG),sacII(CCGCGG),sanDI(GGGWCCC),
sauI(CCTNAGG),scaI(AGTACT),sceI(TAGGGATAACAGGGTAAT),sexAI(ACCWGGT),sfuI(TTCGAA),sgfI(GCGATCGC),sgrAI(CRCCGGYG),
snoI(GTGCAC),snoI(GTGCAC),srfI(GCCCGGGC),sstII(CCGCGG),stuI(AGGCCT),styI(CCWWGG),swaI(ATTTAAAT),
xcmI(CCANNNNNNNNNTGG)